



## SEQUENCE LISTING

<110> Purdue Research Foundation  
Chapple, Clint  
Nair, Ramesh

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<170> PatentIn version 3.3

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 tcgaccccgga cgtgccgttc ggggggtaca agatgagcgg cttcggcaag gacatgggca 1500  
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 cttggctatg atctgatgat gaacagcaca gaaagattaa ttacagtgga aaaaaataac 1620  
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<210> 9  
 <211> 502  
 <212> PRT  
 <213> Oryza sativa

<400> 9

Met Ala Ala Ala Asn Gly Gly Asp Ser Lys Gly Phe Glu Val Pro Lys  
 1 5 10 15

Leu Glu Ile Lys Phe Thr Lys Leu Phe Ile Asn Gly Arg Phe Val Asp  
 20 25 30

Ala Val Ser Gly Lys Thr Phe Glu Thr Arg Asp Pro Arg Thr Gly Glu  
 35 40 45

Val Ile Ala Lys Ile Ala Glu Gly Asp Lys Ala Asp Ile Asp Leu Ala  
 50 55 60

Val Lys Ala Ala Arg Glu Ala Phe Asp His Gly Pro Trp Pro Arg Met  
 65 70 75 80

Ser Gly Phe Ala Arg Gly Arg Ile Leu His Lys Phe Ala Asp Leu Val  
 85 90 95

Glu Gln His Val Glu Glu Leu Ala Ala Leu Asp Thr Val Asp Ala Gly  
 100 105 110

Lys Leu Phe Ala Met Gly Lys Leu Val Asp Ile Pro Gly Gly Ala Asn  
 115 120 125

Leu Leu Arg Tyr Tyr Ala Gly Ala Ala Asp Lys Val His Gly Glu Thr  
 130 135 140

Leu Lys Met Ala Arg Pro Cys His Gly Tyr Thr Leu Lys Glu Pro Val  
 145 150 155 160

Gly Val Val Gly His Ile Val Pro Trp Asn Tyr Pro Thr Thr Met Phe  
 165 170 175

Phe Phe Lys Ala Ser Pro Ala Leu Ala Ala Gly Cys Thr Met Val Val  
 180 185 190

Lys Pro Ala Glu Gln Thr Pro Leu Ser Ala Leu Phe Tyr Ala His Leu  
 195 200 205

Ala Lys Leu Ala Gly Val Pro Asp Gly Val Leu Asn Val Val Pro Gly  
 210 215 220

Phe Gly Pro Thr Ala Gly Ala Ala Ile Ser Ser His Met Asp Ile Asp  
 225 230 235 240

Lys Val Ser Phe Thr Gly Ser Thr Glu Val Gly Arg Leu Val Met Glu  
 245 250 255

Ala Ala Ala Lys Ser Asn Leu Lys Pro Val Ser Leu Glu Leu Gly Gly  
 260 265 270

Lys Ser Pro Val Ile Val Phe Asp Asp Ala Asp Leu Asp Thr Ala Val  
 275 280 285

Asn Leu Val His Met Ala Ser Tyr Thr Asn Lys Gly Glu Ile Cys Val  
 290 295 300

Ala Gly Ser Arg Ile Tyr Val Gln Glu Gly Ile Tyr Asp Ala Phe Val  
 305 310 315 320

Lys Lys Ala Thr Glu Met Ala Lys Lys Ser Val Val Gly Asp Pro Phe  
 325 330 335

Asn Pro Arg Val His Gln Gly Pro Gln Ile Asp Lys Glu Gln Tyr Glu  
 340 345 350

Lys Ile Leu Lys Tyr Ile Asp Ile Gly Lys Arg Glu Gly Ala Thr Leu  
 355 360 365

Val Thr Gly Gly Lys Pro Cys Gly Glu Asn Gly Tyr Tyr Ile Glu Pro  
 370 375 380

Thr Ile Phe Thr Asp Val Lys Glu Glu Met Ser Ile Ala Gln Glu Glu  
 385 390 395 400

Ile Phe Gly Pro Val Met Ala Leu Met Lys Phe Lys Thr Val Glu Glu  
 405 410 415

Ala Ile Gln Lys Ala Asn Ser Thr Arg Tyr Gly Leu Ala Ala Gly Ile  
 420 425 430

Val Thr Lys Asn Ile Asp Val Ala Asn Thr Val Ser Arg Ser Ile Arg  
 435 440 445

Ala Gly Ala Ile Trp Ile Asn Cys Tyr Leu Gly Phe Asp Pro Asp Val  
 450 455 460

Pro Phe Gly Gly Tyr Lys Met Ser Gly Phe Gly Lys Asp Met Gly Met  
 465 470 475 480

Asp Ala Leu Glu Lys Tyr Leu His Thr Lys Ala Val Val Thr Pro Leu  
 485 490 495

Tyr Asn Thr Pro Trp Leu  
 500

<210> 10

<211> 1855

<212> DNA

<213> Oryza sativa

<400> 10

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ggggcttctt gcttggatca cttcacagat tcagcgctgc accggccgcc gctgccaccg 180

ccgcagccac tgaggagccg atccagccgc cggtaggacgt gaagtacacc aagctcctca 240



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ccggcgatgt cattgcccgc gtggccgagg gcgacgcgga ggacgtcaac cgcgccgtcg	360
ccgccgcccgc ccgggccttc gacgagggcc cgtggccgcg gatgaccgcc tacgagcggg	420
gcaggggtgtt gctgcgggtc gcggacctga tcgagcagca cgccgatgag atcgcggcgc	480
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tggcgcggtta catgcgggtac tacggcgggt gggcggacaa gatccacggc ctcgctcgtc	600
cggcggatgg gccacaccac gtgcagggtc tacacgagcc catcggcgtg gccgggcaga	660
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gcgatgaata atgggttaa atcgggcaatct tttgtacaaa aaaaaaaaaa aaaaaa	1855

<210> 11  
 <211> 553  
 <212> PRT  
 <213> Oryza sativa

<400> 11

Met Ala Ala Arg Arg Ala Ala Ser Ser Leu Leu Ser Arg Gly Leu Ile  
 1 5 10 15

Ala Arg Pro Ser Ala Ala Ser Ser Thr Gly Asp Ser Ala Ile Leu Gly  
 20 25 30

Ala Gly Ser Ala Arg Gly Phe Leu Pro Gly Ser Leu His Arg Phe Ser  
 35 40 45

Ala Ala Pro Ala Ala Ala Ala Thr Ala Ala Ala Thr Glu Glu Pro Ile  
 50 55 60

Gln Pro Pro Val Asp Val Lys Tyr Thr Lys Leu Leu Ile Asn Gly Asn  
 65 70 75 80

Phe Val Asp Ala Ala Ser Gly Lys Thr Phe Ala Thr Val Asp Pro Arg  
 85 90 95

Thr Gly Asp Val Ile Ala Arg Val Ala Glu Gly Asp Ala Glu Asp Val  
 100 105 110

Asn Arg Ala Val Ala Ala Ala Arg Arg Ala Phe Asp Glu Gly Pro Trp  
 115 120 125

Pro Arg Met Thr Ala Tyr Glu Arg Cys Arg Val Leu Leu Arg Phe Ala  
 130 135 140

Asp Leu Ile Glu Gln His Ala Asp Glu Ile Ala Ala Leu Glu Thr Trp  
 145 150 155 160

Asp Gly Gly Lys Thr Leu Glu Gln Thr Thr Gly Thr Glu Val Pro Met  
 165 170 175

Val Ala Arg Tyr Met Arg Tyr Tyr Gly Gly Trp Ala Asp Lys Ile His  
 180 185 190

Gly Leu Val Val Pro Ala Asp Gly Pro His His Val Gln Val Leu His  
 195 200 205

Glu Pro Ile Gly Val Ala Gly Gln Ile Ile Pro Trp Asn Phe Pro Leu  
 210 215 220

Leu Met Phe Ala Trp Lys Val Gly Pro Ala Leu Ala Cys Gly Asn Ala  
 225 230 235 240

Val Val Leu Lys Thr Ala Glu Gln Thr Pro Leu Ser Ala Leu Phe Val  
 245 250 255

Ala Ser Leu Leu His Glu Ala Gly Leu Pro Asp Gly Val Leu Asn Val  
 260 265 270

Val Ser Gly Phe Gly Pro Thr Ala Gly Ala Ala Leu Ser Ser His Met  
 275 280 285

Gly Val Asp Lys Leu Ala Phe Thr Gly Ser Thr Gly Thr Gly Lys Ile  
 290 295 300

Val Leu Glu Leu Ala Ala Arg Ser Asn Leu Lys Pro Val Thr Leu Glu  
 305 310 315 320

Leu Gly Gly Lys Ser Pro Phe Ile Val Met Asp Asp Ala Asp Val Asp  
 325 330 335

Gln Ala Val Glu Leu Ala His Arg Ala Leu Phe Phe Asn Gln Gly Gln  
 340 345 350

Cys Cys Cys Ala Gly Ser Arg Thr Phe Val His Glu Arg Val Tyr Asp  
 355 360 365

Glu Phe Val Glu Lys Ala Arg Ala Arg Ala Leu Gln Arg Val Val Gly  
 370 375 380

Asp Pro Phe Arg Thr Gly Val Glu Gln Gly Pro Gln Ile Asp Gly Glu  
 385 390 395 400

Gln Phe Lys Lys Ile Leu Gln Tyr Val Lys Ser Gly Val Asp Ser Gly  
 405 410 415

Ala Thr Leu Val Ala Gly Gly Asp Arg Ala Gly Ser Arg Gly Phe Tyr  
 420 425 430

Ile Gln Pro Thr Val Phe Ala Asp Val Glu Asp Glu Met Lys Ile Ala  
 435 440 445

Gln Glu Glu Ile Phe Gly Pro Val Gln Ser Ile Leu Lys Phe Ser Thr  
 450 455 460

Val Glu Glu Val Val Arg Arg Ala Asn Ala Thr Pro Tyr Gly Leu Ala  
 465 470 475 480

Ala Gly Val Phe Thr Gln Arg Leu Asp Ala Ala Asn Thr Leu Ala Arg  
 485 490 495

Ala Leu Arg Val Gly Thr Val Trp Val Asn Thr Tyr Asp Val Phe Asp  
 500 505 510

Ala Ala Val Pro Phe Gly Gly Tyr Lys Met Ser Gly Val Gly Arg Glu  
 515 520 525

Lys Gly Val Tyr Ser Leu Arg Asn Tyr Leu Gln Thr Lys Ala Val Val  
 530 535 540

Thr Pro Ile Lys Asp Ala Ala Trp Leu  
 545 550

<210> 12  
 <211> 2115  
 <212> DNA  
 <213> Oryza sativa

<400> 12  
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 catcccttcc attccattac tgaccttggc tgctgcggct gcagtgcaga gggggtttgg 120  
 tgggtgcggtt gatttgagca ataaattctc taggggggag ggaggatatcg gtcattggctg 180  
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 ccgccgcctc gcctgctgtc ccctctgcgc tccgcagggc agatgggaca caaggattgt 300  
 tgccgggaat ccttcagagg ttcagcactg cagcagtagc agaggagccc atatcacccc 360  
 cagtccaagt gaactacact cagctcctca ttgatggaaa attcgttgat tcagcatctg 420  
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tgcacgagcc cattgggtgc gcaggtcaga tcatcccatg gaactttccg cttctgatgt	840
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agcaaaactcc tctgtctgct ctatctgctt ctaagctggt gcatgaggct ggactcccag	960
acggtgttgt taacgtggta tctggttttg gacctactgc tgggtgctgct cttgctagtc	1020
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ttgctcaaga agagatatctt ggccctgtgc agtccattct gaagttcaat gatctgaacg	1560
aggtcatcaa gagggcaaat gcaagccagt acgggctggc tgctggggtc ttcaccaaca	1620
acctgaacac ggccaacacc ctgacccgcg cgctcagggt cgggaccgtg tgggtgaact	1680
gcttcgacgt cttcgacgcc gcgatcccgt tcggcggata caagcagagc ggcacggga	1740
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tcaagaacgc cgcgtgggtt taaacacata gatgtttgga catttcagaa ctggggaaga	1860
aataggtata atcttatgga cggatgcgaa aatggcgata aattatggcg ataagattat	1920
gatgatgatg atgaagaaga agaagaggag gaggaagaac agctgaaata agcttgtcct	1980
agcatggggc tggcattgtc tctaataaac cttgtgggtt gtgctcatgt tactgatgga	2040
gtatatgtga gaagcagatt tatgttcatt atgaaatata tatcgcttgt ttgggataaa	2100
aaaaaaaaa aaaaa	2115

<210> 13  
 <211> 549  
 <212> PRT  
 <213> Oryza sativa

<400> 13

Met Ala Ala Ala Ala Ala Arg Arg Gly Ser Ser Leu Leu Ser Arg Cys  
 1 5 10 15

Leu Leu Ser Arg Pro Ala Ala Ala Ser Pro Ala Val Pro Ser Ala  
 20 25 30

Leu Arg Arg Ala Asp Gly Thr Gln Gly Leu Leu Pro Gly Ile Leu Gln  
 35 40 45

Arg Phe Ser Thr Ala Ala Val Ala Glu Glu Pro Ile Ser Pro Pro Val  
 50 55 60

Gln Val Asn Tyr Thr Gln Leu Leu Ile Asp Gly Lys Phe Val Asp Ser  
 65 70 75 80

Ala Ser Gly Lys Thr Phe Pro Thr Leu Asp Pro Arg Thr Gly Glu Leu  
 85 90 95

Ile Ala His Val Ala Glu Gly Asp Ala Glu Asp Ile Asn Arg Ala Val  
 100 105 110

His Ala Ala Arg Lys Ala Phe Asp Glu Gly Pro Trp Pro Lys Met Thr  
 115 120 125

Ala Tyr Glu Arg Ser Arg Ile Leu Leu Arg Phe Ala Asp Leu Ile Glu  
 130 135 140

Lys His Asn Asp Glu Ile Ala Ala Leu Glu Thr Trp Asp Asn Gly Lys  
 145 150 155 160

Pro Tyr Ala Gln Ala Ala Asn Ile Glu Val Pro Met Val Ala Arg Leu  
 165 170 175

Met Arg Tyr Tyr Ala Gly Trp Ala Asp Lys Ile His Gly Leu Val Val  
 180 185 190

Pro Ala Asp Gly Pro His His Val Gln Val Leu His Glu Pro Ile Gly  
 195 200 205

Val Ala Gly Gln Ile Ile Pro Trp Asn Phe Pro Leu Leu Met Phe Ala  
 210 215 220

Trp Lys Val Gly Pro Ala Leu Ala Cys Gly Asn Thr Val Val Leu Lys  
 225 230 235 240

Thr Ala Glu Gln Thr Pro Leu Ser Ala Leu Phe Ala Ser Lys Leu Leu  
 245 250 255

His Glu Ala Gly Leu Pro Asp Gly Val Val Asn Val Val Ser Gly Phe  
 260 265 270

Gly Pro Thr Ala Gly Ala Ala Leu Ala Ser His Met Asp Val Asp Lys  
 275 280 285

Ile Ala Phe Thr Gly Ser Thr Asp Thr Gly Lys Val Val Leu Glu Leu  
 290 295 300

Ala Ala Arg Ser Asn Leu Lys Ser Val Thr Leu Glu Leu Gly Gly Lys  
 305 310 315 320

Ser Pro Phe Ile Ile Met Asp Asp Ala Asp Val Asp His Ala Val Glu  
 325 330 335

Leu Ala His Phe Ala Leu Phe Phe Asn Gln Gly Gln Cys Cys Cys Ala  
 340 345 350

Gly Ser Arg Thr Phe Val His Glu Arg Ile Tyr Asp Glu Phe Val Glu  
 355 360 365

Lys Ala Lys Ala Arg Ala Leu Lys Arg Val Val Gly Asp Pro Phe Lys  
 370 375 380

Asn Gly Val Glu Gln Gly Pro Gln Ile Asp Asp Glu Gln Phe Asn Lys  
 385 390 395 400

Ile Leu Arg Tyr Ile Lys Tyr Gly Val Asp Ser Gly Ala Asn Leu Val  
 405 410 415

Thr Gly Gly Asp Arg Leu Gly Asp Lys Gly Tyr Tyr Ile Gln Pro Thr  
 420 425 430

Ile Phe Ser Asp Val Gln Asp Asn Met Arg Ile Ala Gln Glu Glu Ile  
 435 440 445

Phe Gly Pro Val Gln Ser Ile Leu Lys Phe Asn Asp Leu Asn Glu Val  
 450 455 460

Ile Lys Arg Ala Asn Ala Ser Gln Tyr Gly Leu Ala Ala Gly Val Phe  
 465 470 475 480

Thr Asn Asn Leu Asn Thr Ala Asn Thr Leu Thr Arg Ala Leu Arg Val  
 485 490 495

Gly Thr Val Trp Val Asn Cys Phe Asp Val Phe Asp Ala Ala Ile Pro  
 500 505 510

Phe Gly Gly Tyr Lys Gln Ser Gly Ile Gly Arg Glu Lys Gly Ile Asp  
 515 520 525

Ser Leu Lys Asn Tyr Leu Gln Val Lys Ala Val Val Thr Pro Ile Lys  
 530 535 540

Asn Ala Ala Trp Leu  
 545

<210> 14  
 <211> 1757  
 <212> DNA  
 <213> Zea mays

<400> 14  
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 gtcgacctcg ccgtcaaggc cgcccgggag gccttcgaca acgggcccctg gcccaggatg 300  
 acgggatacg agcgtggtcg gatcctccac aggttcgcgg acctgatcga cgagcacgtg 360  
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 cgggacatcc cgggcgccgc gcacctgctg cgctactacg ccggcgccgc cgacaagggtg 480  
 cacggcgcca cgctcaagat ggcgcagcgg atgcacgggt acacgctcaa ggagcccgtg 540  
 ggcgtgggtg gccacatcgt gccctggaac taccacacca ccatgttctt cttcaaggta 600



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 gtcgtgccgg gattcggggc cacggccggg gccgccgtcg ccgcccacat ggacgtcgac 780  
 aaggtcagct tcaccgggtc cacggagggtc ggccgcctcg tcatgagggc cgcggccgag 840  
 agcaacctca agcccgtgtc gctcgagctg ggccggcaagt ctcccgtcat cgtcttcgac 900  
 gacgccgacc tcgacatggc cgttaacctc gtcaacttcg ccacctacac caacaagggc 960  
 gagatctgtg tggccggcac acgcatctac gtgcaggaag ggatctacga cgagtctgtg 1020  
 aagaaggccg ccgagctcgc cagcaagtcc gtggtcggag acccgttcaa cccgagtgtc 1080  
 agccagggcc cccaggttga caaggaccag tacgagaagg tcctcaggta cattgacatc 1140  
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 gaaatctttg ggccggtgat ggctctcatg aaattcaaga ccgtggagga ggtgatccag 1320  
 aaagcgaaca acaccggta cggcctggcc gccggcatcg tgaccaagaa catcgacgtc 1380  
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 ccatggctct gaccgaccga cctctcatcc tgtccgatga acagttcaac atcacaacaa 1620  
 agaagaaaca tgtcttgtaa gatactctc caaaggatcg ggtgcctgta gctgtactct 1680  
 tacacctgca tggattgatg tcttgatgat gtagtgcaat gtagcattca gaacaataaa 1740  
 gacatgtttc ggactgc 1757

<210> 15  
 <211> 503  
 <212> PRT  
 <213> Zea mays

<400> 15

Met Ala Thr Ala Asn Gly Ser Ser Lys Gly Ser Phe Glu Val Pro Lys  
 1 5 10 15

Val Glu Val Arg Phe Thr Lys Leu Phe Ile Asp Gly Lys Phe Val Asp  
 20 25 30

Ala Val Ser Gly Lys Thr Phe Glu Thr Arg Asp Pro Arg Thr Gly Glu  
 35 40 45

Val Ile Ala Ser Ile Ala Glu Gly Gly Lys Ala Asp Val Asp Leu Ala  
50 55 60

Val Lys Ala Ala Arg Glu Ala Phe Asp Asn Gly Pro Trp Pro Arg Met  
65 70 75 80

Thr Gly Tyr Glu Arg Gly Arg Ile Leu His Arg Phe Ala Asp Leu Ile  
85 90 95

Asp Glu His Val Glu Glu Leu Ala Ala Leu Asp Thr Val Asp Ala Gly  
100 105 110

Lys Leu Phe Ala Val Gly Lys Ala Arg Asp Ile Pro Gly Ala Ala His  
115 120 125

Leu Leu Arg Tyr Tyr Ala Gly Ala Ala Asp Lys Val His Gly Ala Thr  
130 135 140

Leu Lys Met Ala Gln Arg Met His Gly Tyr Thr Leu Lys Glu Pro Val  
145 150 155 160

Gly Val Val Gly His Ile Val Pro Trp Asn Tyr Pro Thr Thr Met Phe  
165 170 175

Phe Phe Lys Val Gly Pro Ala Leu Ala Ala Gly Cys Ala Val Val Val  
180 185 190

Lys Pro Ala Glu Gln Thr Pro Leu Ser Ala Leu Phe Tyr Ala His Leu  
195 200 205

Ala Arg Glu Ala Gly Val Pro Ala Gly Val Leu Asn Val Val Pro Gly  
210 215 220

Phe Gly Pro Thr Ala Gly Ala Ala Val Ala Ala His Met Asp Val Asp  
225 230 235 240

Lys Val Ser Phe Thr Gly Ser Thr Glu Val Gly Arg Leu Val Met Arg  
245 250 255

Ala Ala Ala Glu Ser Asn Leu Lys Pro Val Ser Leu Glu Leu Gly Gly  
 260 265 270

Lys Ser Pro Val Ile Val Phe Asp Asp Ala Asp Leu Asp Met Ala Val  
 275 280 285

Asn Leu Val Asn Phe Ala Thr Tyr Thr Asn Lys Gly Glu Ile Cys Val  
 290 295 300

Ala Gly Thr Arg Ile Tyr Val Gln Glu Gly Ile Tyr Asp Glu Phe Val  
 305 310 315 320

Lys Lys Ala Ala Glu Leu Ala Ser Lys Ser Val Val Gly Asp Pro Phe  
 325 330 335

Asn Pro Ser Val Ser Gln Gly Pro Gln Val Asp Lys Asp Gln Tyr Glu  
 340 345 350

Lys Val Leu Arg Tyr Ile Asp Ile Gly Lys Arg Glu Gly Ala Thr Leu  
 355 360 365

Val Thr Gly Gly Lys Pro Cys Gly Asp Asn Lys Gly Tyr Tyr Ile Glu  
 370 375 380

Pro Thr Ile Phe Thr Asp Val Lys Asp Asp Met Thr Ile Ala Gln Asp  
 385 390 395 400

Glu Ile Phe Gly Pro Val Met Ala Leu Met Lys Phe Lys Thr Val Glu  
 405 410 415

Glu Val Ile Gln Lys Ala Asn Asn Thr Arg Tyr Gly Leu Ala Ala Gly  
 420 425 430

Ile Val Thr Lys Asn Ile Asp Val Ala Asn Thr Val Ser Arg Ser Ile  
 435 440 445

Arg Ala Gly Ala Ile Trp Ile Asn Cys Tyr Phe Ala Phe Asp Pro Asp  
 450 455 460

Ala Pro Phe Gly Gly Tyr Lys Met Ser Gly Phe Gly Lys Asp Met Gly  
 465 470 475 480

Met Asp Ala Leu Asp Lys Tyr Leu Gln Thr Lys Thr Val Val Thr Pro  
 485 490 495

Leu Tyr Asn Thr Pro Trp Leu  
 500

<210> 16  
 <211> 1952  
 <212> DNA  
 <213> Zea mays

<400> 16  
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 cgagtgaggg ggcagaggcc acaaaacaga gagtacccaa acgatcgatc tgtgcatctc 120  
 cccgtccgtc ccgcaaccat ctaattcaga agcagacatc aatggcgagc aacggctgca 180  
 acggcaacgg caacggcaac ggcaacggca aggcggctcc ggcgggtgtg gtggtaccgg 240  
 agatcaagtt caccaagctc ttcattcaacg gcgagttcgt cgacgccgcc tccggcaaga 300  
 cattcgatac cagggaccca cggaccggcg acgtgctggc ccacgtagca gaggcagaca 360  
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<400> 17

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Leu Phe Ile Asn Gly Glu Phe Val Asp Ala Ala Ser Gly Lys Thr Phe  
 35 40 45

Asp Thr Arg Asp Pro Arg Thr Gly Asp Val Leu Ala His Val Ala Glu  
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Ala Asp Lys Ala Asp Val Asp Leu Ala Val Lys Ser Ala Arg Asp Ala  
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Phe Glu His Gly Lys Trp Pro Arg Met Ser Gly Tyr Glu Arg Gly Arg  
 85 90 95

Ile Met Ser Lys Leu Ala Asp Leu Val Glu Gln His Thr Glu Glu Leu  
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 Gln Gly Tyr Thr Leu Lys Glu Pro Ile Gly Val Val Gly Val Ile Ile  
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 Asp Gly Val Ile Asn Val Val Pro Gly Phe Gly Pro Thr Ala Gly Ala  
 225 230 235 240  
 Ala Leu Ala Ser His Met Asp Val Asp Ser Val Ala Phe Thr Gly Ser  
 245 250 255  
 Thr Glu Val Gly Arg Leu Ile Met Glu Ser Ala Ala Arg Ser Asn Leu  
 260 265 270  
 Lys Thr Val Ser Leu Glu Leu Gly Gly Lys Ser Pro Leu Ile Ile Phe  
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 Asp Asp Ala Asp Val Asp Met Ala Val Asn Leu Ser Arg Leu Ala Val  
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 Phe Phe Asn Lys Gly Glu Val Cys Val Ala Gly Ser Arg Val Tyr Val  
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 Gln Glu Gly Ile Tyr Asp Glu Phe Val Lys Lys Ala Val Glu Ala Ala  
 325 330 335

Arg Ser Trp Lys Val Gly Asp Pro Phe Asp Val Thr Ser Asn Met Gly  
 340 345 350

Pro Gln Val Asp Lys Asp Gln Phe Glu Arg Val Leu Lys Tyr Ile Glu  
 355 360 365

His Gly Lys Ser Glu Gly Ala Thr Leu Leu Thr Gly Gly Lys Pro Ala  
 370 375 380

Ala Asp Lys Gly Tyr Tyr Ile Glu Pro Thr Ile Phe Val Asp Val Thr  
 385 390 395 400

Glu Asp Met Lys Ile Ala Gln Glu Glu Ile Phe Gly Pro Val Met Ser  
 405 410 415

Leu Met Lys Phe Lys Thr Val Asp Glu Val Ile Glu Lys Ala Asn Cys  
 420 425 430

Thr Arg Tyr Gly Leu Ala Ala Gly Ile Val Thr Lys Ser Leu Asp Val  
 435 440 445

Ala Asn Arg Val Ser Arg Ser Val Arg Ala Gly Thr Val Trp Val Asn  
 450 455 460

Cys Tyr Phe Ala Phe Asp Pro Asp Ala Pro Phe Gly Gly Tyr Lys Met  
 465 470 475 480

Ser Gly Phe Gly Arg Asp Gln Gly Leu Ala Ala Met Asp Lys Tyr Leu  
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Gln Val Lys Ser Val Ile Thr Ala Leu Pro Asp Ser Pro Trp Tyr  
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<211> 2195

<212> DNA

<213> Zea mays

<400> 18

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actgcgcctg cggaggatcg gaggaaccag tagcggaggc ttcgattttc ggcgggcgca 240

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<212> PRT  
<213> Zea mays

<400> 19

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Thr Val Pro Ala Asp Gly Met His Arg Leu Leu Pro Gly Val Leu Gln  
35 40 45

Arg Phe Ser Thr Ala Ala Ala Val Glu Glu Pro Ile Thr Pro Ser Val  
50 55 60

His Val Asn Tyr Thr Lys Leu Leu Ile Asn Gly Asn Phe Val Asp Ser  
65 70 75 80

Ala Ser Gly Lys Thr Phe Pro Thr Leu Asp Pro Arg Thr Gly Glu Val  
85 90 95

Ile Ala His Val Ala Glu Gly Asp Ala Glu Asp Ile Asn Arg Ala Val  
100 105 110

Ala Ala Ala Arg Lys Ala Phe Asp Glu Gly Pro Trp Pro Lys Met Thr  
115 120 125

Ala Tyr Glu Arg Ser Arg Ile Leu Leu Arg Phe Ala Asp Leu Ile Glu  
130 135 140

Lys His Asn Asp Glu Leu Ala Ala Leu Glu Thr Trp Asp Asn Gly Lys  
145 150 155 160

Pro Tyr Glu Gln Ala Ala Gln Ile Glu Val Pro Met Val Ala Arg Leu  
165 170 175

Met Arg Tyr Tyr Ala Gly Trp Ala Asp Lys Ile His Gly Leu Ile Val  
 180 185 190

Pro Ala Asp Gly Pro His His Val Gln Ile Leu His Glu Pro Ile Gly  
 195 200 205

Val Ala Gly Gln Ile Ile Pro Trp Asn Phe Pro Leu Leu Met Tyr Ala  
 210 215 220

Trp Lys Val Gly Pro Ala Leu Ala Cys Gly Asn Thr Leu Val Leu Lys  
 225 230 235 240

Thr Ala Glu Gln Thr Pro Leu Ser Ala Leu Tyr Ile Ser Lys Leu Leu  
 245 250 255

His Glu Ala Gly Leu Pro Glu Gly Val Val Asn Val Val Ser Gly Phe  
 260 265 270

Gly Pro Thr Ala Gly Ala Ala Leu Ala Ser His Met Asp Val Asp Lys  
 275 280 285

Ile Ala Phe Thr Gly Ser Thr Asp Thr Gly Lys Ile Ile Leu Glu Leu  
 290 295 300

Ala Ala Lys Ser Asn Leu Lys Thr Val Thr Leu Glu Leu Gly Gly Lys  
 305 310 315 320

Ser Pro Phe Ile Ile Met Asp Asp Ala Asp Val Asp His Ala Val Glu  
 325 330 335

Leu Ala His Phe Ala Leu Phe Phe Asn Gln Gly Gln Cys Cys Cys Ala  
 340 345 350

Gly Ser Arg Thr Phe Val His Glu Arg Val Tyr Asp Glu Phe Val Glu  
 355 360 365

Lys Ala Lys Ala Arg Ala Leu Lys Arg Val Val Gly Asp Pro Phe Arg  
 370 375 380

Lys Gly Val Glu Gln Gly Pro Gln Ile Asp Asp Glu Gln Phe Asn Lys  
 385 390 395 400

Ile Leu Arg Tyr Ile Arg Tyr Gly Val Asp Gly Gly Ala Thr Leu Val  
405 410 415

Thr Gly Gly Asp Arg Leu Gly Asp Lys Gly Phe Tyr Ile Gln Pro Thr  
420 425 430

Ile Phe Ser Asp Val Gln Asp Gly Met Lys Ile Ala Gln Glu Glu Ile  
435 440 445

Phe Gly Pro Val Gln Ser Ile Leu Lys Phe Lys Asp Leu Asn Glu Val  
450 455 460

Ile Lys Arg Ala Asn Ala Ser Gln Tyr Gly Leu Ala Ala Gly Val Phe  
465 470 475 480

Thr Asn Ser Leu Asp Thr Ala Asn Thr Leu Thr Arg Ala Leu Arg Ala  
485 490 495

Gly Thr Val Trp Val Asn Cys Phe Asp Val Phe Asp Ala Ala Ile Pro  
500 505 510

Phe Gly Gly Tyr Lys Met Ser Gly Ile Gly Arg Glu Lys Gly Val Asp  
515 520 525

Ser Leu Lys Asn Tyr Leu Gln Val Lys Ala Val Val Thr Pro Ile Lys  
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Asn Ala Ala Trp Leu  
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<212> DNA  
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 <211> 550  
 <212> PRT  
 <213> Zea mays

<400> 21

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Leu Leu Thr Lys Pro Ser Pro Ser Pro Ala Ser Ala Ala Gly Asn Asn  
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Ser Ala Leu Leu Gly Ser Gly Ala Ala Ala Leu His Arg Phe Ser Thr  
 35 40 45

Ala Pro Ala Ser Ala Ala Ala Ala Ala Glu Glu Pro Ile Gln Pro Ala  
 50 55 60

Val Glu Val Lys His Thr Gln Leu Leu Ile Asn Gly Asn Phe Val Asp  
 65 70 75 80

Ala Ala Ser Gly Lys Thr Phe Pro Thr Leu Asp Pro Arg Thr Gly Glu  
 85 90 95

Val Ile Ala Arg Val Ala Glu Gly Asp Ser Glu Asp Ile Asp Arg Ala  
 100 105 110

Val Ala Ala Ala Arg Arg Ala Phe Asp Glu Gly Pro Trp Pro Arg Met  
 115 120 125

Thr Ala Tyr Asp Arg Cys Arg Val Leu Leu Arg Phe Ala Asp Leu Ile  
 130 135 140

Glu Arg His Ala Glu Glu Val Ala Ala Leu Glu Thr Trp Asp Asn Gly  
 145 150 155 160

Lys Thr Leu Ala Gln Ala Ala Gly Ala Glu Val Pro Met Val Ala Arg  
 165 170 175

Cys Val Arg Tyr Tyr Ala Gly Trp Ala Asp Lys Ile His Gly Leu Val  
 180 185 190

Ala Pro Ala Asp Gly Ala His His Val Gln Val Leu His Glu Pro Val  
 195 200 205

Gly Val Ala Gly Gln Ile Ile Pro Trp Asn Phe Pro Leu Leu Met Phe  
 210 215 220

Ala Trp Lys Val Gly Pro Ala Leu Ala Cys Gly Asn Thr Val Val Leu  
 225 230 235 240

Lys Thr Ala Glu Gln Thr Pro Leu Ser Ala Leu Tyr Val Ala Asn Leu  
 245 250 255

Leu His Glu Ala Gly Leu Pro Glu Gly Val Leu Asn Val Val Ser Gly  
 260 265 270

Phe Gly Pro Thr Ala Gly Ala Ala Leu Ser Ser His Met Gly Val Asp  
 275 280 285

Lys Leu Ala Phe Thr Gly Ser Thr Gly Thr Gly Gln Ile Val Leu Glu  
 290 295 300

Leu Ala Ala Arg Ser Asn Leu Lys Pro Val Thr Leu Glu Leu Gly Gly  
 305 310 315 320

Lys Ser Pro Phe Ile Val Met Asp Asp Ala Asp Val Asp Gln Ala Val  
 325 330 335

Glu Leu Ala His Gln Ala Val Phe Phe Asn Gln Gly Gln Cys Cys Cys  
 340 345 350

Ala Gly Ser Arg Thr Phe Val His Glu Arg Val Tyr Asp Glu Phe Val  
 355 360 365

Glu Lys Ser Lys Ala Arg Ala Leu Lys Arg Val Val Gly Asp Pro Phe  
 370 375 380

Arg Asp Gly Val Glu Gln Gly Pro Gln Ile Asp Gly Glu Gln Phe Asn  
 385 390 395 400

Lys Ile Leu Arg Tyr Val Gln Ser Gly Val Asp Ser Gly Ala Thr Leu  
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Val Ala Gly Gly Asp Arg Val Gly Asp Arg Gly Phe Tyr Ile Gln Pro  
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Thr Val Phe Ala Asp Ala Lys Asp Glu Met Lys Ile Ala Arg Glu Glu  
435 440 445

Ile Phe Gly Pro Val Gln Thr Ile Leu Lys Phe Ser Gly Val Glu Glu  
450 455 460

Val Ile Arg Arg Ala Asn Ala Thr Pro Tyr Gly Leu Ala Ala Gly Val  
465 470 475 480

Phe Thr Arg Ser Leu Asp Ala Ala Asn Thr Leu Ser Arg Ala Leu Arg  
485 490 495

Ala Gly Thr Val Trp Val Asn Cys Tyr Asp Val Phe Asp Ala Thr Ile  
500 505 510

Pro Phe Gly Gly Tyr Lys Met Ser Gly Val Gly Arg Glu Lys Gly Ile  
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Tyr Ala Leu Arg Asn Tyr Leu Gln Thr Lys Ala Val Val Thr Pro Ile  
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Lys Asn Pro Ala Trp Leu  
545 550

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<211> 2071  
<212> DNA  
<213> Nicotiana tabacum

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<210> 23  
 <211> 542  
 <212> PRT  
 <213> *Nicotiana tabacum*

<400> 23

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Ser His Leu Gly Arg Ile Ala Ala Tyr Gln Tyr Ser Thr Ala Ala Ala  
 35 40 45

Ile Glu Glu Pro Ile Lys Pro Ala Val Asn Val Glu His Thr Lys Leu  
 50 55 60

Phe Ile Asn Gly Gln Phe Val Asp Ala Ala Ser Gly Lys Thr Phe Pro  
 65 70 75 80

Thr Leu Asp Pro Arg Thr Gly Glu Val Ile Ala His Val Ala Glu Gly  
 85 90 95

Asp Ala Glu Asp Ile Asn Arg Ala Val Ala Ala Ala Arg Lys Ala Phe  
 100 105 110

Asp Glu Gly Pro Trp Pro Lys Met Asn Ala Tyr Glu Arg Ser Lys Ile  
 115 120 125

Phe Val Arg Leu Ala Asp Leu Ile Glu Lys His Asn Asp Gln Ile Ala  
 130 135 140

Thr Leu Glu Thr Trp Asp Thr Gly Lys Pro Tyr Glu Gln Ala Ala Lys  
 145 150 155 160

Ile Glu Val Pro Met Val Val Arg Leu Leu Arg Tyr Tyr Ala Gly Trp  
 165 170 175

Ala Asp Lys Ile His Gly Met Thr Ile Pro Ala Asp Gly Pro Tyr His  
 180 185 190

Val Gln Thr Leu His Glu Pro Ile Gly Val Ala Gly Gln Ile Ile Pro  
 195 200 205

Trp Asn Phe Pro Leu Leu Met Phe Ser Trp Lys Ile Gly Pro Ala Leu  
 210 215 220

Ala Cys Gly Asn Thr Val Val Leu Lys Thr Ala Glu Gln Thr Pro Leu  
 225 230 235 240

Ser Ala Phe Tyr Val Ala His Leu Leu Gln Glu Ala Gly Leu Pro Glu  
 245 250 255

Gly Val Leu Asn Ile Ile Ser Gly Phe Gly Pro Thr Ala Gly Ala Pro  
 260 265 270

Leu Cys Ser His Met Asp Val Asp Lys Leu Ala Phe Thr Gly Ser Thr  
 275 280 285

Asp Thr Gly Lys Ala Ile Leu Ser Leu Ala Ala Lys Ser Asn Leu Lys  
 290 295 300

Pro Val Thr Leu Glu Leu Gly Gly Lys Ser Pro Phe Ile Val Cys Glu  
 305 310 315 320

Asp Ala Asp Ile Asp Thr Ala Val Glu Gln Ala His Phe Ala Leu Phe  
 325 330 335

Phe Asn Gln Gly Gln Cys Cys Cys Ala Gly Ser Arg Thr Phe Val His  
 340 345 350

Glu Lys Val Tyr Asp Glu Phe Leu Glu Lys Ala Lys Ala Arg Ala Leu  
 355 360 365

Lys Arg Thr Val Gly Asp Pro Phe Lys Ser Gly Thr Glu Gln Gly Pro  
 370 375 380

Gln Ile Asp Ser Lys Gln Phe Asp Lys Ile Met Asn Tyr Ile Arg Ser  
 385 390 395 400

Gly Ile Asp Ser Gly Ala Thr Leu Glu Thr Gly Gly Glu Arg Leu Gly  
 405 410 415

Glu Arg Gly Tyr Tyr Ile Lys Pro Thr Val Phe Ser Asn Val Lys Asp  
 420 425 430

Asp Met Leu Ile Ala Gln Asp Glu Ile Phe Gly Pro Val Gln Ser Ile  
 435 440 445

Leu Lys Phe Lys Asp Val Asp Asp Val Ile Arg Arg Ala Asn Asn Ser  
 450 455 460

Arg Tyr Gly Leu Ala Ala Gly Val Phe Thr Gln Asn Ile Asp Thr Ala  
 465 470 475 480

Asn Thr Leu Thr Arg Ala Leu Arg Val Gly Thr Val Trp Val Asn Cys  
 485 490 495

Phe Asp Thr Phe Asp Ala Thr Ile Pro Phe Gly Gly Tyr Lys Met Ser  
 500 505 510

Gly His Gly Arg Glu Lys Gly Glu Tyr Ser Leu Lys Asn Tyr Leu Gln  
 515 520 525

Val Lys Ala Val Val Thr Pro Leu Lys Asn Pro Ala Trp Leu  
 530 535 540

<210> 24  
 <211> 1713  
 <212> DNA  
 <213> Hordeum vulgare

<400> 24  
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 agggaacggg cgacgtcgat ggcggcagcg aacggcggcc aggggtttga ggtgccggaa 120  
 ctggacatca agttcaccaa gctcttcacg aatggccagt tcgtcgacgc agcttcaggc 180  
 aagacgttcg agaccggga cccacgcacc ggcgaggtga tcgccaggat cgccgagggga 240  
 gacaaggccg acatcgacct cgccgtgaag gccgcccgcg acgccttcga caacggcccc 300  
 tggcccagaa tgcccggctg cgcaaggga aggatcctgc acaagttcgc cgacctggtc 360  
 gaccagcacg tggaggagct ggcggcgtg gacacggtgg acgccggcaa gctgttccag 420  
 atgggcaagc tggaggagat ccccgaggc gccaacctgc tccggtacta cgccggtgcc 480  
 gccgacaaga tccacggcga gacgctcaag atggcgcggc cgctgcacgg gtacacgctc 540  
 aaggagcccg tcggcgctgt gggccacatc gtgccctgga actacccac caccatgttc 600

ttcttcaagg tcagccccgc gctcgccgcc ggggtgcacca tggtcgtcaa gccggccgag 660  
 cagacgcccc tctccgcgct cttctacgct cacctcgcca aggaggccgg gatccccgac 720  
 ggcgtcctca acgtcgtgcc cggctttggc ccgacggccg gtgcggccat ggcttctcac 780  
 atggacatcg acaagatcag cttcacggga tccacggagg tggggcggct ggatcatgcag 840  
 gcggcgcccc tgagcaacct caagcccgtc tcgctggagc tggggggcaa gtccccgac 900  
 atcgtgtttg acgacgccga tgttgacatg gccgtgagcc tcgttaacat ggccacctac 960  
 accaacaagg gcgagatctg cgtcgctggc acgcgcatat acgtgcagga agggatctac 1020  
 gacgcctttg tgaacaagtc agtggagctt gccaaagaaat ccgtggtcgg agatcctttc 1080  
 aaccgaacg tacatcaagg tcctcaggtt gacaagaatc aatacgagaa ggtcctcaag 1140  
 tacatcgacg tcggtaagag cgaaggcgcc accctactca ccggagggaa ggcctgcagc 1200  
 gacaagggtt actacatcga gcccgccatc ttcaccgacg tcaaggatga catgtcgatt 1260  
 gcgcaagagg aaatcttcgg gccgggtgatg gctctcatga aattcaagac aatggaggag 1320  
 gtgattcaga aggcgaacag caccgcctat ggcttgcccg ccggcggtgtt gaccaagaac 1380  
 atcgacacca tgaacaccgt gtcgcggctg gtcagggtccg gggtcgtctg ggttaactgc 1440  
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 gacatgggca cggatgccct cgacaagtac ctgcacacca agacgggtgtt cactccactc 1560  
 tacaacacgc cctggttgtg atctggacgg acatccgacg gaaacgcatg gggaaagatt 1620  
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 ttattacttg tggccaatct ttttcgtggt att 1713

<210> 25  
 <211> 500  
 <212> PRT  
 <213> Hordeum vulgare

<400> 25

Met Ala Ala Ala Asn Gly Gly Gln Gly Phe Glu Val Pro Glu Leu Asp  
 1 5 10 15

Ile Lys Phe Thr Lys Leu Phe Ile Asn Gly Gln Phe Val Asp Ala Ala  
 20 25 30

Ser Gly Lys Thr Phe Glu Thr Arg Asp Pro Arg Thr Gly Glu Val Ile  
 35 40 45

Ala	Arg	Ile	Ala	Glu	Gly	Asp	Lys	Ala	Asp	Ile	Asp	Leu	Ala	Val	Lys
50						55					60				
Ala	Ala	Arg	Asp	Ala	Phe	Asp	Asn	Gly	Pro	Trp	Pro	Arg	Met	Pro	Gly
65					70					75					80
Cys	Ala	Arg	Ala	Arg	Ile	Leu	His	Lys	Phe	Ala	Asp	Leu	Val	Asp	Gln
				85					90					95	
His	Val	Glu	Glu	Leu	Ala	Ala	Leu	Asp	Thr	Val	Asp	Ala	Gly	Lys	Leu
			100					105					110		
Phe	Gln	Met	Gly	Lys	Leu	Val	Asp	Ile	Pro	Gly	Gly	Ala	Asn	Leu	Leu
		115					120					125			
Arg	Tyr	Tyr	Ala	Gly	Ala	Ala	Asp	Lys	Ile	His	Gly	Glu	Thr	Leu	Lys
	130						135				140				
Met	Ala	Arg	Pro	Leu	His	Gly	Tyr	Thr	Leu	Lys	Glu	Pro	Val	Gly	Val
145					150					155					160
Val	Gly	His	Ile	Val	Pro	Trp	Asn	Tyr	Pro	Thr	Thr	Met	Phe	Phe	Phe
				165					170					175	
Lys	Val	Ser	Pro	Ala	Leu	Ala	Ala	Gly	Cys	Thr	Met	Val	Val	Lys	Pro
			180					185					190		
Ala	Glu	Gln	Thr	Pro	Leu	Ser	Ala	Leu	Phe	Tyr	Ala	His	Leu	Ala	Lys
		195					200					205			
Glu	Ala	Gly	Ile	Pro	Asp	Gly	Val	Leu	Asn	Val	Val	Pro	Gly	Phe	Gly
	210					215					220				
Pro	Thr	Ala	Gly	Ala	Ala	Met	Ala	Ser	His	Met	Asp	Ile	Asp	Lys	Ile
225					230					235					240
Ser	Phe	Thr	Gly	Ser	Thr	Glu	Val	Gly	Arg	Leu	Val	Met	Gln	Ala	Ala
				245					250					255	
Ala	Leu	Ser	Asn	Leu	Lys	Pro	Val	Ser	Leu	Glu	Leu	Gly	Gly	Lys	Ser
			260					265					270		
Pro	Ile	Ile	Val	Phe	Asp	Asp	Ala	Asp	Val	Asp	Met	Ala	Val	Ser	Leu
	275						280					285			

Val Asn Met Ala Thr Tyr Thr Asn Lys Gly Glu Ile Cys Val Ala Gly  
 290 295 300

Thr Arg Ile Tyr Val Gln Glu Gly Ile Tyr Asp Ala Phe Val Asn Lys  
 305 310 315 320

Ser Val Glu Leu Ala Lys Lys Ser Val Val Gly Asp Pro Phe Asn Pro  
 325 330 335

Asn Val His Gln Gly Pro Gln Val Asp Lys Asn Gln Tyr Glu Lys Val  
 340 345 350

Leu Lys Tyr Ile Asp Val Gly Lys Ser Glu Gly Ala Thr Leu Leu Thr  
 355 360 365

Gly Gly Lys Ala Cys Ser Asp Lys Gly Tyr Tyr Ile Glu Pro Ala Ile  
 370 375 380

Phe Thr Asp Val Lys Asp Asp Met Ser Ile Ala Gln Glu Glu Ile Phe  
 385 390 395 400

Gly Pro Val Met Ala Leu Met Lys Phe Lys Thr Met Glu Glu Val Ile  
 405 410 415

Gln Lys Ala Asn Ser Thr Arg Tyr Gly Leu Ala Ala Gly Val Val Thr  
 420 425 430

Lys Asn Ile Asp Thr Met Asn Thr Val Ser Arg Ser Val Arg Ser Gly  
 435 440 445

Val Val Trp Val Asn Cys Tyr Phe Ala Phe Asp Pro Asp Ala Pro Phe  
 450 455 460

Gly Gly Cys Lys Met Ser Gly Phe Gly Lys Asp Met Gly Thr Asp Ala  
 465 470 475 480

Leu Asp Lys Tyr Leu His Thr Lys Thr Val Val Thr Pro Leu Tyr Asn  
 485 490 495

Thr Pro Trp Leu  
 500

<210> 26  
 <211> 2212  
 <212> DNA  
 <213> Hordeum vulgare

<400> 26  
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 ccctaccatt tactactgag cctctgaacc cggaggacga gaagaattga ttgctgatcc 120  
 ggcgcaaacc aacagattct tcttgctcc gccgagatca tcatcatggc tgetgccgcc 180  
 acgaggaggg ccgcctcctc gctcgtctcc cgtgcctgc tctccaggcc cgcagcttcc 240  
 cccgcgcgtg tccccctgc gctccgcagg gcagatgggg cacgtggatt gttgcctgga 300  
 ctctttcaga ggttcggcac tgcagcagca gcagaggaac ccatctcgcc ttctgtccaa 360  
 gtgggcgaga cacagctcct catcaacggc aaattcgttg atgctgcac tggcaagact 420  
 ttcccgactc tggaccctcg caccggggag gtgattgccc gtgtgtctga aggagatgcc 480  
 gaagatgttg accgtgcagt tgttgcggcc cgcaaggcat tcgatgaagg gccatggcca 540  
 aagatgactg cctatgagag gtcccgatt cttttgcgat ttgctgattt gatagagaaa 600  
 cacaatgatg aaattgctgc actggagacg tgggacaacg ggaagcccta tgagcaagct 660  
 gccacatcg aagtgccaat gcttgctcgg cttatgcggt actatgcagg ctggactgac 720  
 aagatccatg gcctcatcgt accggctgat ggccgcacc atgtacagg tctgcatgag 780  
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 aaagttggcc ctgctttggc ctgtgggaac actattgttc tcaagaccgc tgaacaaact 900  
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 gcacggagca atcttaaggc agtgacactg gagctaggag gcaagtctcc ttttatcgtc 1140  
 atggatgatg cagatattga ccaagctgtt gagcttgccg attttgcgct gtttttcaac 1200  
 caggggcaat gctgctgcgc tgggtctcgc acgttcgtac atgagcgtgt ttatgatgag 1260  
 tttgttgaga agtcaaaggc tcgtgctttg aagcgtgtag ttggtgatcc attcaggaaa 1320  
 ggtgttgagc agggctctca gattgatgat gagcaattca agaagatctt gcgctacatt 1380  
 aagtcgggtg tcgacagtgg agccaccctt gtgacgggtg gtgacaagtt gggtgacaaa 1440  
 ggttactaca tccagccaac aattttctca gatgtgcagg atgacatgaa gatagcccag 1500  
 gaggagatat tcgggcctgt tcagtcaatc ttcaagttca atgacctcaa cgaggatgc 1560

aagagggcga acgcaagcca gtacggattg gccgccggcg tttttaccaa caacctggac 1620  
acggccaaca ccttgacgcg tgccctcagg gccggcacga tctgggtgaa ctgctttgac 1680  
atcttcgatg ccgcgatccc cttcggcggg tacaagatga gcggcatcgg tagggagaag 1740  
ggcatcgaca gcctgaagaa ctacctgcaa gtcaaggcgg tcgtcaccgc gcttaagaac 1800  
cctgcgtggt tgtgagcata gcacacctat ggtcttctga gtctgagata ccggacaacg 1860  
tgaagacgca gggacaattg gatgagaaaa aaagaagatg atgatgataa caacgatgag 1920  
gatctctaataagccattcc ttcattgggca gccagccacc gtctctaatt agtatcatat 1980  
gtgatttggt ttcttttgtc aaccgcggca agacatatat gttgtatggt gtagcaacat 2040  
tatgttgatt atagcttggt ggaaaaattc tctggttgca gttaatcaac ttcttttgat 2100  
cagttgttgt tctgcgacac atatgaagct aatggtgttt cctatcctag ttaatccatg 2160  
tccttggtga tcatcaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 2212

<210> 27  
<211> 549  
<212> PRT  
<213> Hordeum vulgare

<400> 27

Met Ala Ala Ala Ala Thr Arg Arg Ala Ala Ser Ser Leu Val Ser Arg  
1 5 10 15

Cys Leu Leu Ser Arg Pro Ala Ala Ser Pro Ala Ala Val Pro Ser Ala  
20 25 30

Leu Arg Arg Ala Asp Gly Ala Arg Gly Leu Leu Pro Gly Leu Leu Gln  
35 40 45

Arg Phe Gly Thr Ala Ala Ala Ala Glu Glu Pro Ile Ser Pro Ser Val  
50 55 60

Gln Val Gly Glu Thr Gln Leu Leu Ile Asn Gly Lys Phe Val Asp Ala  
65 70 75 80

Ala Ser Gly Lys Thr Phe Pro Thr Leu Asp Pro Arg Thr Gly Glu Val  
85 90 95

Ile Ala Arg Val Ser Glu Gly Asp Ala Glu Asp Val Asp Arg Ala Val  
100 105 110



Val Ala Ala Arg Lys Ala Phe Asp Glu Gly Pro Trp Pro Lys Met Thr  
 115 120 125

Ala Tyr Glu Arg Ser Arg Ile Leu Leu Arg Phe Ala Asp Leu Ile Glu  
 130 135 140

Lys His Asn Asp Glu Ile Ala Ala Leu Glu Thr Trp Asp Asn Gly Lys  
 145 150 155 160

Pro Tyr Glu Gln Ala Ala His Ile Glu Val Pro Met Leu Ala Arg Leu  
 165 170 175

Met Arg Tyr Tyr Ala Gly Trp Thr Asp Lys Ile His Gly Leu Ile Val  
 180 185 190

Pro Ala Asp Gly Pro His His Val Gln Val Leu His Glu Pro Ile Gly  
 195 200 205

Val Val Gly Gln Ile Ile Pro Trp Asn Phe Pro Leu Leu Met Tyr Gly  
 210 215 220

Trp Lys Val Gly Pro Ala Leu Ala Cys Gly Asn Thr Ile Val Leu Lys  
 225 230 235 240

Thr Ala Glu Gln Thr Pro Leu Ser Ala Leu Tyr Val Ser Lys Leu Leu  
 245 250 255

His Glu Ala Gly Leu Pro Glu Gly Val Leu Asn Ile Ile Ser Gly Phe  
 260 265 270

Gly Pro Thr Ala Gly Ala Ala Leu Ala Gly His Met Asp Val Asp Lys  
 275 280 285

Ile Ala Phe Thr Gly Ser Thr Asp Thr Gly Lys Val Ile Leu Glu Leu  
 290 295 300

Ser Ala Arg Ser Asn Leu Lys Ala Val Thr Leu Glu Leu Gly Gly Lys  
 305 310 315 320

Ser Pro Phe Ile Val Met Asp Asp Ala Asp Ile Asp Gln Ala Val Glu  
 325 330 335

Leu Ala His Phe Ala Leu Phe Phe Asn Gln Gly Gln Cys Cys Cys Ala  
 340 345 350

Gly Ser Arg Thr Phe Val His Glu Arg Val Tyr Asp Glu Phe Val Glu  
355 360 365

Lys Ser Lys Ala Arg Ala Leu Lys Arg Val Val Gly Asp Pro Phe Arg  
370 375 380

Lys Gly Val Glu Gln Gly Pro Gln Ile Asp Asp Glu Gln Phe Lys Lys  
385 390 395 400

Ile Leu Arg Tyr Ile Lys Ser Gly Val Asp Ser Gly Ala Thr Leu Val  
405 410 415

Thr Gly Gly Asp Lys Leu Gly Asp Lys Gly Tyr Tyr Ile Gln Pro Thr  
420 425 430

Ile Phe Ser Asp Val Gln Asp Asp Met Lys Ile Ala Gln Glu Glu Ile  
435 440 445

Phe Gly Pro Val Gln Ser Ile Phe Lys Phe Asn Asp Leu Asn Glu Val  
450 455 460

Ile Lys Arg Ala Asn Ala Ser Gln Tyr Gly Leu Ala Ala Gly Val Phe  
465 470 475 480

Thr Asn Asn Leu Asp Thr Ala Asn Thr Leu Thr Arg Ala Leu Arg Ala  
485 490 495

Gly Thr Ile Trp Val Asn Cys Phe Asp Ile Phe Asp Ala Ala Ile Pro  
500 505 510

Phe Gly Gly Tyr Lys Met Ser Gly Ile Gly Arg Glu Lys Gly Ile Asp  
515 520 525

Ser Leu Lys Asn Tyr Leu Gln Val Lys Ala Val Val Thr Ala Leu Lys  
530 535 540

Asn Pro Ala Trp Leu  
545

<210> 28  
 <211> 1700  
 <212> DNA  
 <213> *Medicago truncatula*

<400> 28  
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 ttgggaaaca cacaagatg actctacctt cttccaatgg caagactaat ctctctctag 120  
 agattcccac catcaagttc accaaactct tcatcaatgg agaatttggt gattcccttt 180  
 caggaaaaga gtttgagaca atagatccaa gaagtggaga ggtgatagca aaaattgcag 240  
 agggaaacgaa agaagacatt gatgttgctg taaaagcggc acgtgtcgct ttcgatgatg 300  
 gtccatggcc tcgtatgccc ggttttgtaa gagcaaaaat aatgctgaaa tgggcagact 360  
 taattgatca aaacatagaa gaaatagcag cattagatac aatagatgct ggaaaactat 420  
 acactttctg caaagctggt gacattcctg gagtagcaaa tataatacgt tacctatgcc 480  
 ggtgctgctg ataaaattca cggcaagggt ttaaaacctg ctcgaggagt gcacgcatat 540  
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 atgtttgctg ctaagggtgc tctgtctttg gctgctgggt gtactatggg tcttaagcct 660  
 gctgaacaaa cacctctctc tgccttggtt tatgctcatc ttgctaagga ggctggaatt 720  
 ccagatggag tgctcaatgt agtacctgga tttggtgcaa ctgcaggagc tgcaataagc 780  
 tcacacatgg acattgataa ggtagtctt accggttcaa cagaagtagg acgcgaaata 840  
 atggtatctg cagctagaag taatttgaaa ccagtttcac ttgaattagg aggaaaatca 900  
 cccctcttaa tttttgatga tgcgtatggt aataaagctg ctgaacttgc tctccttggc 960  
 attttattta ataagggaga aatttggtgt gcgggttctc gtgtggttgt tcaagaagga 1020  
 atctatgatg aatttgagaa gaagttggtg gagaaagcaa aagcttgggt tggttggtgat 1080  
 ccttttgatc ctaaagttca acaagggcct caggttgaca agaagcaatt tgaaaaaatt 1140  
 ctttctaca ttgagcatgg aaagaatgat ggcgcaacct ttttgacagg tggtaaaaaa 1200  
 attggagaca agggttacta cattgagcct acaattttct caaatgttaa ggaggacatg 1260  
 cgtatagcac aagatgaaat atttggccct gtcatggcac tcatgaagtt caagactatt 1320  
 gaggaagcaa tcaaaagtgc aaacaatata aaatatggct tagcagcagg aattgtgaca 1380  
 aagaatttg atatagcaaa cactgtgtca aggtccatta gagcaggaat tatttggtatt 1440  
 aattgctact ttgcctttgg aaatgatatt ccttatggag gttacaagat gagtgggttt 1500  
 ggaagagatt ttggattgga atcattacat aaatatattgc aagttaaatc tgttgtaact 1560

cccatttaca attctccttg gctttgaatg ttctttgtat ttgggttatg tgtatttgag 1620  
 agtgaacaaa tggacctttt ccatgtataa ttcatacataa taataacatt ataagatctt 1680  
 atgttatgtt acatccaatc 1700

<210> 29  
 <211> 502  
 <212> PRT  
 <213> Medicago truncatula

<400> 29

Met Thr Leu Pro Ser Ser Asn Gly Lys Thr Asn Leu Ser Leu Glu Ile  
 1 5 10 15

Pro Thr Ile Lys Phe Thr Lys Leu Phe Ile Asn Gly Glu Phe Val Asp  
 20 25 30

Ser Leu Ser Gly Lys Glu Phe Glu Thr Ile Asp Pro Arg Ser Gly Glu  
 35 40 45

Val Ile Ala Lys Ile Ala Glu Gly Thr Lys Glu Asp Ile Asp Val Ala  
 50 55 60

Val Lys Ala Ala Arg Val Ala Phe Asp Asp Gly Pro Trp Pro Arg Met  
 65 70 75 80

Pro Gly Phe Val Arg Ala Lys Ile Met Leu Lys Trp Ala Asp Leu Ile  
 85 90 95

Asp Gln Asn Ile Glu Glu Ile Ala Ala Leu Asp Thr Ile Asp Ala Gly  
 100 105 110

Lys Leu Tyr Thr Phe Cys Lys Ala Val Asp Ile Pro Gly Val Ala Asn  
 115 120 125

Ile Ile Arg Tyr Leu Ala Gly Ala Ala Asp Lys Ile His Gly Lys Val  
 130 135 140

Leu Lys Pro Ala Arg Glu Leu His Ala Tyr Thr Leu Met Glu Pro Ile  
 145 150 155 160

Gly Val Val Gly His Ile Ile Pro Trp Asn Phe Pro Ser Thr Met Phe  
 165 170 175

Ala Ala Lys Val Ala Pro Ala Leu Ala Ala Gly Cys Thr Met Val Leu  
 180 185 190

Lys Pro Ala Glu Gln Thr Pro Leu Ser Ala Leu Phe Tyr Ala His Leu  
 195 200 205

Ala Lys Glu Ala Gly Ile Pro Asp Gly Val Leu Asn Val Val Pro Gly  
 210 215 220

Phe Gly Ala Thr Ala Gly Ala Ala Ile Ser Ser His Met Asp Ile Asp  
 225 230 235 240

Lys Val Ser Phe Thr Gly Ser Thr Glu Val Gly Arg Glu Ile Met Val  
 245 250 255

Ser Ala Ala Arg Ser Asn Leu Lys Pro Val Ser Leu Glu Leu Gly Gly  
 260 265 270

Lys Ser Pro Leu Leu Ile Phe Asp Asp Ala Asp Val Asn Lys Ala Ala  
 275 280 285

Glu Leu Ala Leu Leu Gly Ile Leu Phe Asn Lys Gly Glu Ile Cys Val  
 290 295 300

Ala Gly Ser Arg Val Phe Val Gln Glu Gly Ile Tyr Asp Glu Phe Glu  
 305 310 315 320

Lys Lys Leu Val Glu Lys Ala Lys Ala Trp Val Val Gly Asp Pro Phe  
 325 330 335

Asp Pro Lys Val Gln Gln Gly Pro Gln Val Asp Lys Lys Gln Phe Glu  
 340 345 350

Lys Ile Leu Ser Tyr Ile Glu His Gly Lys Asn Asp Gly Ala Thr Leu  
 355 360 365

Leu Thr Gly Gly Lys Lys Ile Gly Asp Lys Gly Tyr Tyr Ile Glu Pro  
 370 375 380

Thr Ile Phe Ser Asn Val Lys Glu Asp Met Arg Ile Ala Gln Asp Glu  
 385 390 395 400

Ile Phe Gly Pro Val Met Ala Leu Met Lys Phe Lys Thr Ile Glu Glu  
 405 410 415

Ala Ile Lys Ser Ala Asn Asn Thr Lys Tyr Gly Leu Ala Ala Gly Ile  
 420 425 430

Val Thr Lys Asn Leu Asp Ile Ala Asn Thr Val Ser Arg Ser Ile Arg  
 435 440 445

Ala Gly Ile Ile Trp Ile Asn Cys Tyr Phe Ala Phe Gly Asn Asp Ile  
 450 455 460

Pro Tyr Gly Gly Tyr Lys Met Ser Gly Phe Gly Arg Asp Phe Gly Leu  
 465 470 475 480

Glu Ser Leu His Lys Tyr Leu Gln Val Lys Ser Val Val Thr Pro Ile  
 485 490 495

Tyr Asn Ser Pro Trp Leu  
 500

<210> 30  
 <211> 1484  
 <212> DNA  
 <213> *Medicago truncatula*

<400> 30  
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 gattttgtgg attcggttac aggcaagaca tttgaaacaa tagatccaag aacaggagaa 120  
 gttatagcaa ggatcagcga aggaaccaa gaagacattg atgttgctgt aaaggcagct 180  
 cgttatgcat ttgactttgg tccttgcccc cgctgctg gtgctgaaag agcaaaactt 240  
 atgatgaaat ttgcggacct aattgatgaa aacatagaag agctagcagc acttgatgcc 300  
 attgatgcag gaaagttgta ccatatgtgt aaggetcttg acattccctc agcagcaaat 360  
 acacttcggt actatgcagg tgcagctgat aaaattcatg gagaggtatt aaaagttgca 420  
 agagagttcc atgcttatac attgatggaa ccaattggtg ttgatggaca cattattcct 480  
 tggaactttc cacttccct gttctttgtc aagggtagcc cttgcttaac tgctgggtgc 540  
 accatggtcg tcaaacctgc tgagcaaaca cctctatctg ctttgtttta tgctcatcta 600  
 gctaaattgg ctggaatccc agatggagtg atcaatgtag taccgggatt tggagctact 660  
 gctggtgctg cagtgaagtc acacatggac attgatgcgg ttagctttac tggttcaaca 720  
 caaactgggc gtgagataat gcaagctgca gctaagagta acttgaaaca tgtttcactt 780  
 gaattaggag gcaagtcacc cctcataata tttgatgatg ctgatattga caaagctact 840

gaacttgctc tattagggcat cctattttaac aagggagaag tgtgtgttgc aagttcacgt 900  
 gtgtttgttc aagaagggat ctatgatgaa tttgagaaaa aattggtaga aaaggctaaa 960  
 acttggggtca ttggagaccc atttgatcct aaagttcagc aaggacctca agttgacaag 1020  
 aaacaatttg aaaaagttct ttcatatata gagcatggga agaaagaagg agctaccctt 1080  
 ttgactgggg gtaaaacagt gggaaacaaa ggatactata ttgaaccaac aattttctcc 1140  
 aatataaagg atgatatggg tatagcacag gatgaaatat ttggctctgt gatggcactg 1200  
 aagaagttta agactattga ggaagcaatt aagagtgcata ataatacaag atatggacta 1260  
 gcagcaggta ttgtgacaaa gaatttggat attgcaaaca cagtgtcaag atccattcgt 1320  
 gcaggcacta tttggataaa ctgttatttt gcttttggag atgatattcc ttttggagga 1380  
 tataaaatga gtggatttgg aagagattat ggattagaag cccttcacaa gtatctacaa 1440  
 gttaaactctg ttgttactcc catttataat tctccctggc tcta 1484

<210> 31  
 <211> 494  
 <212> PRT  
 <213> Medicago truncatula

<400> 31

Met Thr Gly Pro Val Asn Gly Glu Pro Thr Ile Lys Phe Thr Lys Leu  
 1 5 10 15

Phe Ile Asp Gly Asp Phe Val Asp Ser Val Thr Gly Lys Thr Phe Glu  
 20 25 30

Thr Ile Asp Pro Arg Thr Gly Glu Val Ile Ala Arg Ile Ser Glu Gly  
 35 40 45

Thr Lys Glu Asp Ile Asp Val Ala Val Lys Ala Ala Arg Tyr Ala Phe  
 50 55 60

Asp Phe Gly Pro Trp Pro Arg Leu Pro Gly Ala Glu Arg Ala Lys Leu  
 65 70 75 80

Met Met Lys Phe Ala Asp Leu Ile Asp Glu Asn Ile Glu Glu Leu Ala  
 85 90 95

Ala Leu Asp Ala Ile Asp Ala Gly Lys Leu Tyr His Met Cys Lys Ala  
 100 105 110

Leu Asp Ile Pro Ser Ala Ala Asn Thr Leu Arg Tyr Tyr Ala Gly Ala  
 115 120 125

Ala Asp Lys Ile His Gly Glu Val Leu Lys Val Ala Arg Glu Phe His  
 130 135 140

Ala Tyr Thr Leu Met Glu Pro Ile Gly Val Asp Gly His Ile Ile Pro  
 145 150 155 160

Trp Asn Phe Pro Thr Ser Leu Phe Phe Val Lys Gly Ser Pro Cys Leu  
 165 170 175

Thr Ala Gly Cys Thr Met Val Val Lys Pro Ala Glu Gln Thr Pro Leu  
 180 185 190

Ser Ala Leu Phe Tyr Ala His Leu Ala Lys Leu Ala Gly Ile Pro Asp  
 195 200 205

Gly Val Ile Asn Val Val Pro Gly Phe Gly Ala Thr Ala Gly Ala Ala  
 210 215 220

Val Ser Ser His Met Asp Ile Asp Ala Val Ser Phe Thr Gly Ser Thr  
 225 230 235 240

Gln Thr Gly Arg Glu Ile Met Gln Ala Ala Ala Lys Ser Asn Leu Lys  
 245 250 255

His Val Ser Leu Glu Leu Gly Gly Lys Ser Pro Leu Ile Ile Phe Asp  
 260 265 270

Asp Ala Asp Ile Asp Lys Ala Thr Glu Leu Ala Leu Leu Gly Ile Leu  
 275 280 285

Phe Asn Lys Gly Glu Val Cys Val Ala Ser Ser Arg Val Phe Val Gln  
 290 295 300

Glu Gly Ile Tyr Asp Glu Phe Glu Lys Lys Leu Val Glu Lys Ala Lys  
 305 310 315 320

Thr Trp Val Ile Gly Asp Pro Phe Asp Pro Lys Val Gln Gln Gly Pro  
 325 330 335

Gln Val Asp Lys Lys Gln Phe Glu Lys Val Leu Ser Tyr Ile Glu His  
 340 345 350



Gly Lys Lys Glu Gly Ala Thr Leu Leu Thr Gly Gly Lys Thr Val Gly  
 355 360 365

Asn Lys Gly Tyr Tyr Ile Glu Pro Thr Ile Phe Ser Asn Ile Lys Asp  
 370 375 380

Asp Met Val Ile Ala Gln Asp Glu Ile Phe Gly Pro Val Met Ala Leu  
 385 390 395 400

Lys Lys Phe Lys Thr Ile Glu Glu Ala Ile Lys Ser Ala Asn Asn Thr  
 405 410 415

Arg Tyr Gly Leu Ala Ala Gly Ile Val Thr Lys Asn Leu Asp Ile Ala  
 420 425 430

Asn Thr Val Ser Arg Ser Ile Arg Ala Gly Thr Ile Trp Ile Asn Cys  
 435 440 445

Tyr Phe Ala Phe Gly Asp Asp Ile Pro Phe Gly Gly Tyr Lys Met Ser  
 450 455 460

Gly Phe Gly Arg Asp Tyr Gly Leu Glu Ala Leu His Lys Tyr Leu Gln  
 465 470 475 480

Val Lys Ser Val Val Thr Pro Ile Tyr Asn Ser Pro Trp Leu  
 485 490

<210> 32  
 <211> 1511  
 <212> DNA  
 <213> Medicago truncatula

<400> 32  
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 aagtataaca agctcttcat caatggagat tttgtcgatt ctgtatcagg aagcacattt 120  
 gaaacaatag acccaagaac aggagatgtg attgcaagaa taagtgaagg agcaaaagaa 180  
 gacattgaaa ttgcagttaa agcagcacgt gaagcatttg attcaggtcc atggccccgg 240  
 atgtctgggtg ttgaacgtgc gaaaataatg atgaaatttg cagaactaat tgatgaaaac 300  
 atagaagaac tagcaacatt agatgcaatt gatgctggca aggtgtactt tatcaacaag 360  
 gcttttgaaa ttccttcagc agcaaataca ctacgttact atgcaggtgc tgctgataaa 420  
 attcatgggtg aggtattaaa atcttctggc caattccatg catacacact gatggaacca 480

attggtgttg tgggacacat cattccatgg aatgctccca ctatgggtttt cttcaccaaaa 540  
 gttagccctt ccttagctgc tgggtgcacc atggtttctca aacctgctga acaaacacct 600  
 ctttctgctt tgttttatgc ccatctagct aagctggctg ggatcccaaa tggagtgtg 660  
 aatgtagtac ccggatttgg tccaactgct ggtgctgcaa tcagctcaca catggacata 720  
 gatgttgca gctttactgg ttcagttgaa gtaggccgtg aaataatgca agctgcagct 780  
 aagagtaatt taaaacatgt ttcacttgaa ttaggaggca agtcacctct cataattttc 840  
 gatgatgcaa acatagacaa agctgttgag ctagctcttt tgggtatcct agctaacaag 900  
 ggagaaaattt gcgttgcatg ttcccggtg tttgttcagg aagggatcta cgatcaagta 960  
 gagaagaagt tgggtggagaa ggcaaaagcc tgggtcattg gagatccttt tgatcctaaa 1020  
 actcaacaag gacctcaggc tgataggaac caattcgaaa aaatcatttc ctatattgag 1080  
 catggaaaga gagaaggagc tacactcttg actggaggta gaagagtggg cagtcagggc 1140  
 tactacattg aacctacaat tttctccaat gtaaaggagg acatgcttat agcacaggat 1200  
 gaaatatttg gccctgtgat ggcaactatg aagttcaaga ctattgagga agccattaag 1260  
 agtgccaaca ataccagata tggcctagca gcaggcattg tgaccaagaa cttggatatt 1320  
 gcaaacactg tttcaaggtc catccgtgca ggcattatct ggatcaactc ttatcttgcc 1380  
 gtgggaagtg acattccttt tggaggatat aaaatgagtg gatttggaag agatcagggg 1440  
 ttagaagctc ttcacaagta cttacaagtt aaatccattg taacacctat ttacaattct 1500  
 ccctggcttt g 1511

<210> 33  
 <211> 503  
 <212> PRT  
 <213> *Medicago truncatula*

<400> 33

Met Thr Asp Leu Asn Ser Ser Asn Gly Asp Asn Ser Ser Leu Phe Lys  
 1 5 10 15

Met Pro Thr Ile Lys Tyr Asn Lys Leu Phe Ile Asn Gly Asp Phe Val  
 20 25 30

Asp Ser Val Ser Gly Ser Thr Phe Glu Thr Ile Asp Pro Arg Thr Gly  
 35 40 45

Asp Val Ile Ala Arg Ile Ser Glu Gly Ala Lys Glu Asp Ile Glu Ile  
 50 55 60

Ala	Val	Lys	Ala	Ala	Arg	Glu	Ala	Phe	Asp	Ser	Gly	Pro	Trp	Pro	Arg	65	70	75	80
Met	Ser	Gly	Val	Glu	Arg	Ala	Lys	Ile	Met	Met	Lys	Phe	Ala	Glu	Leu	85	90	95	
Ile	Asp	Glu	Asn	Ile	Glu	Glu	Leu	Ala	Thr	Leu	Asp	Ala	Ile	Asp	Ala	100	105	110	
Gly	Lys	Val	Tyr	Phe	Ile	Asn	Lys	Ala	Phe	Glu	Ile	Pro	Ser	Ala	Ala	115	120	125	
Asn	Thr	Leu	Arg	Tyr	Tyr	Ala	Gly	Ala	Ala	Asp	Lys	Ile	His	Gly	Glu	130	135	140	
Val	Leu	Lys	Ser	Ser	Gly	Gln	Phe	His	Ala	Tyr	Thr	Leu	Met	Glu	Pro	145	150	155	160
Ile	Gly	Val	Val	Gly	His	Ile	Ile	Pro	Trp	Asn	Ala	Pro	Thr	Met	Val	165	170	175	
Phe	Phe	Thr	Lys	Val	Ser	Pro	Ser	Leu	Ala	Ala	Gly	Cys	Thr	Met	Val	180	185	190	
Leu	Lys	Pro	Ala	Glu	Gln	Thr	Pro	Leu	Ser	Ala	Leu	Phe	Tyr	Ala	His	195	200	205	
Leu	Ala	Lys	Leu	Ala	Gly	Ile	Pro	Asn	Gly	Val	Leu	Asn	Val	Val	Pro	210	215	220	
Gly	Phe	Gly	Pro	Thr	Ala	Gly	Ala	Ala	Ile	Ser	Ser	His	Met	Asp	Ile	225	230	235	240
Asp	Val	Val	Ser	Phe	Thr	Gly	Ser	Val	Glu	Val	Gly	Arg	Glu	Ile	Met	245	250	255	
Gln	Ala	Ala	Ala	Lys	Ser	Asn	Leu	Lys	His	Val	Ser	Leu	Glu	Leu	Gly	260	265	270	
Gly	Lys	Ser	Pro	Leu	Ile	Ile	Phe	Asp	Asp	Ala	Asn	Ile	Asp	Lys	Ala	275	280	285	

Val Glu Leu Ala Leu Leu Gly Ile Leu Ala Asn Lys Gly Glu Ile Cys  
 290 295 300

Val Ala Cys Ser Arg Val Phe Val Gln Glu Gly Ile Tyr Asp Gln Val  
 305 310 315 320

Glu Lys Lys Leu Val Glu Lys Ala Lys Ala Trp Val Ile Gly Asp Pro  
 325 330 335

Phe Asp Pro Lys Thr Gln Gln Gly Pro Gln Ala Asp Arg Asn Gln Phe  
 340 345 350

Glu Lys Ile Ile Ser Tyr Ile Glu His Gly Lys Arg Glu Gly Ala Thr  
 355 360 365

Leu Leu Thr Gly Gly Arg Arg Val Gly Ser Gln Gly Tyr Tyr Ile Glu  
 370 375 380

Pro Thr Ile Phe Ser Asn Val Lys Glu Asp Met Leu Ile Ala Gln Asp  
 385 390 395 400

Glu Ile Phe Gly Pro Val Met Ala Leu Met Lys Phe Lys Thr Ile Glu  
 405 410 415

Glu Ala Ile Lys Ser Ala Asn Asn Thr Arg Tyr Gly Leu Ala Ala Gly  
 420 425 430

Ile Val Thr Lys Asn Leu Asp Ile Ala Asn Thr Val Ser Arg Ser Ile  
 435 440 445

Arg Ala Gly Ile Ile Trp Ile Asn Ser Tyr Leu Ala Val Gly Ser Asp  
 450 455 460

Ile Pro Phe Gly Gly Tyr Lys Met Ser Gly Phe Gly Arg Asp Gln Gly  
 465 470 475 480

Leu Glu Ala Leu His Lys Tyr Leu Gln Val Lys Ser Ile Val Thr Pro  
 485 490 495

Ile Tyr Asn Ser Pro Trp Leu  
 500

<210> 34  
 <211> 1720  
 <212> DNA  
 <213> Glycine max

<400> 34  
 ggcacgagggc gccagcgtct ctacgacaat ctccctttctc tctaactcat aactcagatg 60  
 agtgcctctct ctctaactcc agtagtagcc acggcaattc ctccctcaag atgcccccca 120  
 tcaagttttac caagctcttc atcaatggag atttcgttga ttccatatca ggaaggacat 180  
 ttgagactat agaccccaga aaagaagagg taattgcaag agttagttag ggagataaag 240  
 aagacattga tattgctgtt aaagcagcac gtcaggcatt tgaactgggt ccatggcctc 300  
 gcttgccagg ctctgaaagg gcaaaaatta tgatgaaatg ggcagacctt gttgatgaaa 360  
 atatagaaga actagcagca ttagatacca ttgatgctgg aaagctatac tatattaata 420  
 aggtagcggg aattccttca gctacaaatg cgttacggta ctatgcaggt gctgctgata 480  
 aaattcacgg tgacgtatta aaaatgaacg gggatttcca tgcatataca cttttggaac 540  
 caattggtgt tgtgggacac ataattccat ggaatgcccc cagcctctca tttttcatca 600  
 aggttagccc ttccttagct gcaggctgta ctatggctct caaacctgct gaacaaacac 660  
 ccctctctgc gtggtgttat gctcatataa ctaagggtggc tggaatccca gatggtgtgc 720  
 ttaatatagt acctggattt ggcccaactg ctggcgccagc aataagctca cacatggaca 780  
 tagatgcggc cagttttact ggttcaattg aagtagggcg tgaagtgatg caggctgcag 840  
 ctaggagcaa tttaaaacca gtttcacttg aattaggagg caagtctcct ctcatatttt 900  
 tcaatgacgc ggatatagac aaagctgccc agcttgctct ctttggcatc atgtctaaca 960  
 agggagaaaat ttgtgtggca agttctcggg tgtttgtcca ggaagagatc tatgatgaat 1020  
 ttgagaagaa gttggtggag aaggcaaaat cttgggtcgt tggggatcct tttgatccca 1080  
 aatccctgca agggcctcag gctgacagga accaattgga gaaaatactc tcctatattg 1140  
 aacacggaaa gagagaagga gctacccttt tgaccggagg taatacagtg ggcaacaaag 1200  
 gttactacat agaacctaca attttctgta atgtaaagga ggacatgctt atagcacgag 1260  
 atgaaatatt tggccctgta ctagcgtgta tgaaatttaa gaccatggag gaagcaatta 1320  
 aaagtgctaa caacaccaag tatggcctag cagcaggaat tgtgaccaag aatttgata 1380  
 ctgcaaacac tatgtcaagg tccattcgtg caggcattgt ttggatcaac tgctatttaa 1440  
 ccgtagggag tgacgttctt tttggagggt ataagatgag tggatttgga agagatttg 1500  
 gattgcaggc ccttcataag tacttacaag ttaaattctgt tgtaacacct attcacaatt 1560

ctccttggtt ttgaataatt gaatgtctcc tacatgagca catatgcgtg tcttctctca 1620  
 tttgaaataa attacacttt atttccttat gatgtatgac ttaaaaatac ttagtctctt 1680  
 gtattatgag ttctttgttt tattacaacg ttgttaactt 1720

<210> 35  
 <211> 487  
 <212> PRT  
 <213> Glycine max

<400> 35

Met Pro Pro Ile Lys Phe Thr Lys Leu Phe Ile Asn Gly Asp Phe Val  
 1 5 10 15

Asp Ser Ile Ser Gly Arg Thr Phe Glu Thr Ile Asp Pro Arg Lys Glu  
 20 25 30

Glu Val Ile Ala Arg Val Ser Glu Gly Asp Lys Glu Asp Ile Asp Ile  
 35 40 45

Ala Val Lys Ala Ala Arg Gln Ala Phe Asp Ser Gly Pro Trp Pro Arg  
 50 55 60

Leu Pro Gly Ser Glu Arg Ala Lys Ile Met Met Lys Trp Ala Asp Leu  
 65 70 75 80

Val Asp Glu Asn Ile Glu Glu Leu Ala Ala Leu Asp Thr Ile Asp Ala  
 85 90 95

Gly Lys Leu Tyr Tyr Ile Asn Lys Val Ala Glu Ile Pro Ser Ala Thr  
 100 105 110

Asn Ala Leu Arg Tyr Tyr Ala Gly Ala Ala Asp Lys Ile His Gly Asp  
 115 120 125

Val Leu Lys Met Asn Gly Asp Phe His Ala Tyr Thr Leu Leu Glu Pro  
 130 135 140

Ile Gly Val Val Gly His Ile Ile Pro Trp Asn Ala Pro Ser Leu Ser  
 145 150 155 160

Phe Phe Ile Lys Val Ser Pro Ser Leu Ala Ala Gly Cys Thr Met Val  
 165 170 175

Leu Lys Pro Ala Glu Gln Thr Pro Leu Ser Ala Trp Cys Tyr Ala His  
 180 185 190

Ile Thr Lys Val Ala Gly Ile Pro Asp Gly Val Leu Asn Ile Val Pro  
 195 200 205

Gly Phe Gly Pro Thr Ala Gly Ala Ala Ile Ser Ser His Met Asp Ile  
 210 215 220

Asp Ala Val Ser Phe Thr Gly Ser Ile Glu Val Gly Arg Glu Val Met  
 225 230 235 240

Gln Ala Ala Ala Arg Ser Asn Leu Lys Pro Val Ser Leu Glu Leu Gly  
 245 250 255

Gly Lys Ser Pro Leu Ile Ile Phe Asn Asp Ala Asp Ile Asp Lys Ala  
 260 265 270

Ala Gln Leu Ala Leu Phe Gly Ile Met Ser Asn Lys Gly Glu Ile Cys  
 275 280 285

Val Ala Ser Ser Arg Val Phe Val Gln Glu Glu Ile Tyr Asp Glu Phe  
 290 295 300

Glu Lys Lys Leu Val Glu Lys Ala Lys Ser Trp Val Val Gly Asp Pro  
 305 310 315 320

Phe Asp Pro Lys Ser Leu Gln Gly Pro Gln Ala Asp Arg Asn Gln Leu  
 325 330 335

Glu Lys Ile Leu Ser Tyr Ile Glu His Gly Lys Arg Glu Gly Ala Thr  
 340 345 350

Leu Leu Thr Gly Gly Asn Thr Val Gly Asn Lys Gly Tyr Tyr Ile Glu  
 355 360 365

Pro Thr Ile Phe Cys Asn Val Lys Glu Asp Met Leu Ile Ala Arg Asp  
 370 375 380

Glu Ile Phe Gly Pro Val Leu Ala Leu Met Lys Phe Lys Thr Met Glu  
 385 390 395 400

Glu Ala Ile Lys Ser Ala Asn Asn Thr Lys Tyr Gly Leu Ala Ala Gly  
 405 410 415

Ile Val Thr Lys Asn Leu Asp Thr Ala Asn Thr Met Ser Arg Ser Ile  
420 425 430

Arg Ala Gly Ile Val Trp Ile Asn Cys Tyr Leu Thr Val Gly Ser Asp  
435 440 445

Val Pro Phe Gly Gly Tyr Lys Met Ser Gly Phe Gly Arg Asp Leu Gly  
450 455 460

Leu Gln Ala Leu His Lys Tyr Leu Gln Val Lys Ser Val Val Thr Pro  
465 470 475 480

Ile His Asn Ser Pro Trp Leu  
485

<210> 36  
<211> 1641  
<212> DNA  
<213> Triticum aestivum

<220>  
<221> misc\_feature  
<222> (1546)..(1546)  
<223> n is a, c, g, or t

<220>  
<221> misc\_feature  
<222> (1584)..(1585)  
<223> n is a, c, g, or t

<220>  
<221> misc\_feature  
<222> (1597)..(1597)  
<223> n is a, c, g, or t

<400> 36  
tcggcacgag gctcactcat tctctccacc gaggccaagg gaagggacga gctgaacggg 60  
gcgatggcga tggcggcagc gaacggcgcc aaggggtttg aggtgccgga actggacatc 120  
aagttcacca agctcttcat caatggccag ttcgtcgacg cggcttccgg caagacgttc 180  
gagaccggg acccacgcac cggcgaggtg atcgccaaga tcgccgaggg agacaaggcc 240  
gacatcgacc tcgccgtgaa ggccgcccgc gaggccttcg acaacggccc atggcccaga 300  
atgcccggct gtgcaagggc ccgatcatg cacaggttcg cggacctggt ggaccagcac 360  
gtcgaggagc tggcggcgct ggacacggtg gacgccggca agctattcct gatgggtaag 420  
atgatggaca tccccggagg cgccaacctg ctccgtact acgccggcgc cgccgacaag 480



atccacggcg agacgctcaa gatggcgcg	ccgctccacg gctacacgct caaggagccc	540
gtcggcgctcg tggggccacat cgtgccatgg	aactacccca ccaccatggt cttcttcaag	600
gtcagccccg cgctcgccgc cggctgcacc	atggctgtca agcccgccga gcagacgccc	660
ctctccgcgc tctttctacgc ccacctcgcc	aaggaggccg gcatccccga cggcgttctc	720
aacgtcgtgc ccggatttgg acccacggcc	ggtgccgcca tcgcctctca catggacgtc	780
gacaagatca gcttcacggg atccacggag	gtcgggcggc tggatcatgca ggctgcggcc	840
acgagcaacc taaagcccg	ctcactggag ctggggggca agtccccgt	900
catcggtgtt		
gacgacgccc acgttgacat ggccgtcaac	ctcggttaaca tggccaccta catgaacaag	960
ggcgagatct gcgtcgccgg cacacgcata	tacgtgcagg aagggatcta cgacgccttt	1020
gtgaagaaat cggctcgagct tgccaagaaa	tcgggtggctg gagatccttt caacccaaac	1080
gtacatcaag gccctcaggt tgacaaggat	caatacgaaa aggtgctcaa gtacatcgac	1140
gtcggtaaga gcgaaggcgc caccctcctc	accggaggga agccctgcag cgacaagggt	1200
tactacatcg agcccaccat cttcaccgac	gtcaccgatg acatgtcgat tgcgcaagag	1260
gaaatcttcg gccagtcac ggctctcatg	aaattcaaga cgggtggacga ggtgattcag	1320
aaggccaaca gcacccggta tggcctggcc	gccggcggtg tgaccaagaa catcgacacc	1380
atgaacaccg tgtcgcggtc cgtcaggctc	ggggtcgtct ggggttaactg ctacttcgcc	1440
ttccgacccc cgacccccgt tcggcggtg	caagatgaag cggcttttcg caaggacatg	1500
ggcacggatc tctccgagaa attacctgca	caccaaagac ggtggncact cccgctctac	1560
aacacccctg ggctgttgat gttnnacgga	catcccnacc acaaacaagc acaggcgaaa	1620
acaaatgggg ggagaaagat t		1641

<210> 37  
 <211> 504  
 <212> PRT  
 <213> Triticum aestivum

<220>  
 <221> misc\_feature  
 <222> (495)..(495)  
 <223> Xaa can be any naturally occurring amino acid

<400> 37

Met Ala Met Ala Ala Ala Asn Gly Ala Lys Gly Phe Glu Val Pro Glu  
1 5 10 15

Leu Asp Ile Lys Phe Thr Lys Leu Phe Ile Asn Gly Gln Phe Val Asp  
20 25 30

Ala Ala Ser Gly Lys Thr Phe Glu Thr Arg Asp Pro Arg Thr Gly Glu  
35 40 45

Val Ile Ala Lys Ile Ala Glu Gly Asp Lys Ala Asp Ile Asp Leu Ala  
50 55 60

Val Lys Ala Ala Arg Glu Ala Phe Asp Asn Gly Pro Trp Pro Arg Met  
65 70 75 80

Pro Gly Cys Ala Arg Ala Arg Ile Met His Arg Phe Ala Asp Leu Val  
85 90 95

Asp Gln His Val Glu Glu Leu Ala Ala Leu Asp Thr Val Asp Ala Gly  
100 105 110

Lys Leu Phe Leu Met Gly Lys Met Met Asp Ile Pro Gly Gly Ala Asn  
115 120 125

Leu Leu Arg Tyr Tyr Ala Gly Ala Ala Asp Lys Ile His Gly Glu Thr  
130 135 140

Leu Lys Met Ala Arg Pro Leu His Gly Tyr Thr Leu Lys Glu Pro Val  
145 150 155 160

Gly Val Val Gly His Ile Val Pro Trp Asn Tyr Pro Thr Thr Met Phe  
165 170 175

Phe Phe Lys Val Ser Pro Ala Leu Ala Ala Gly Cys Thr Met Val Val  
180 185 190

Lys Pro Ala Glu Gln Thr Pro Leu Ser Ala Leu Phe Tyr Ala His Leu  
195 200 205

Ala Lys Glu Ala Gly Ile Pro Asp Gly Val Leu Asn Val Val Pro Gly  
210 215 220

Phe Gly Pro Thr Ala Gly Ala Ala Ile Ala Ser His Met Asp Val Asp  
 225 230 235 240

Lys Ile Ser Phe Thr Gly Ser Thr Glu Val Gly Arg Leu Val Met Gln  
 245 250 255

Ala Ala Ala Thr Ser Asn Leu Lys Pro Val Ser Leu Glu Leu Gly Gly  
 260 265 270

Lys Ser Pro Val Ile Val Phe Asp Asp Ala Asp Val Asp Met Ala Val  
 275 280 285

Asn Leu Val Asn Met Ala Thr Tyr Met Asn Lys Gly Glu Ile Cys Val  
 290 295 300

Ala Gly Thr Arg Ile Tyr Val Gln Glu Gly Ile Tyr Asp Ala Phe Val  
 305 310 315 320

Lys Lys Ser Val Glu Leu Ala Lys Lys Ser Val Val Gly Asp Pro Phe  
 325 330 335

Asn Pro Asn Val His Gln Gly Pro Gln Val Asp Lys Asp Gln Tyr Glu  
 340 345 350

Lys Val Leu Lys Tyr Ile Asp Val Gly Lys Ser Glu Gly Ala Thr Leu  
 355 360 365

Leu Thr Gly Gly Lys Pro Cys Ser Asp Lys Gly Tyr Tyr Ile Glu Pro  
 370 375 380

Thr Ile Phe Thr Asp Val Thr Asp Asp Met Ser Ile Ala Gln Glu Glu  
 385 390 395 400

Ile Phe Gly Pro Val Met Ala Leu Met Lys Phe Lys Thr Val Asp Glu  
 405 410 415

Val Ile Gln Lys Ala Asn Ser Thr Arg Tyr Gly Leu Ala Ala Gly Val  
 420 425 430

Val Thr Lys Asn Ile Asp Thr Met Asn Thr Val Ser Arg Ser Val Arg  
 435 440 445

Ser Gly Val Val Trp Val Asn Cys Tyr Phe Ala Phe Arg Pro Pro Thr  
 450 455 460

Pro Val Arg Arg Leu Gln Asp Glu Ala Ala Phe Gly Lys Asp Met Gly  
 465 470 475 480

Thr Asp Leu Ser Glu Lys Leu Pro Ala His Gln Arg Arg Trp Xaa Leu  
 485 490 495

Pro Leu Tyr Asn Thr Pro Gly Leu  
 500

<210> 38  
 <211> 2197  
 <212> DNA  
 <213> Triticum aestivum

<400> 38  
 taccacgcg tccgcatcac tgetccccct ctctcctcag tccccactct cttccccagc 60  
 agctggggac gccctcccat ttactgagcc aagaggagga ggggaagaag aattgattgc 120  
 cgatccggcg cagaccaata aattgttccc gcctccgccg cgagatcatc atggctgctg 180  
 ccgccacgag gagggccgcc tcctcgctcg cctcccgctg cctgctcgcc aggcccgag 240  
 cgtegccgcg cgctgtcccc tccgcgctcc gcagggcaga tgggtgcacgt ggattgttgc 300  
 caggactcct tcagaggttc ggcactgcgg cagcagcaga ggagcccatt tcgccttctg 360  
 tocaagtggg cgagacacag ctccctatca acggcaaatt cggtgatgct gcatctggta 420  
 aaactttccc gactgtggac cctcgcaccg gggaggtgat tgcccgcgtg gccgaaggag 480  
 atgccgaaga tggtgaccgt gcggttgctg ctgcccgcaa ggcattcgat gaagggccat 540  
 ggcccaggat gactgcctat gagagatccc gtattcttct gcggtttgct gatttgatag 600  
 agaaacacaa tgatgatatc gctgcactgg agacgtggga caacgggaag ccctatgagc 660  
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Arg Phe Gly Thr Ala Ala Ala Ala Glu Glu Pro Ile Ser Pro Ser Val  
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Gln Val Gly Glu Thr Gln Leu Leu Ile Asn Gly Lys Phe Val Asp Ala  
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Ala Ser Gly Lys Thr Phe Pro Thr Val Asp Pro Arg Thr Gly Glu Val  
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Lys His Asn Asp Asp Ile Ala Ala Leu Glu Thr Trp Asp Asn Gly Lys  
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Pro Tyr Glu Gln Ala Ala His Ile Glu Val Pro Met Leu Val Arg Leu  
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Pro Ala Asp Gly Pro His His Val Gln Val Leu His Glu Pro Ile Gly  
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Thr Asn Asn Leu Asp Thr Ala Asn Thr Leu Thr Arg Ala Leu Arg Ala  
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